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Shin et al.

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(54) **HIGH RESOLUTION STR ANALYSIS USING
NEXT GENERATION SEQUENCING**

(56) **References Cited**

(71) Applicant: **The Board of Trustees of the Leland
Stanford Junior University**, Stanford,
CA (US)

(72) Inventors: **Giwon Shin**, Stanford, CA (US); **Billy
Tsz Cheong Lau**, Palo Alto, CA (US);
HoJoon Lee, Stanford, CA (US);
Hanlee P. Ji, Stanford, CA (US)

(73) Assignee: **THE BOARD OF TRUSTEES OF
THE LELEAND STANFORD
JUNIOR UNIVERSITY**, Stanford, CA
(US)

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CPC **C12Q 1/6869** (2013.01)

(58) **Field of Classification Search**
None

See application file for complete search history.

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Primary Examiner — Kaijiang Zhang

(74) *Attorney, Agent, or Firm* — James S. Keddie;
Bozicevic, Field & Francis LLP

(57) **ABSTRACT**

A method for analyzing short tandem repeats (STRs) is
described herein. In some embodiments, the method com-
prises: separately digesting two portions of a genomic
sample at sites that are upstream and downstream of an STR;
fragmenting those products; ligating adaptors to the frag-
mentation products; selectively amplifying part of the top
strand but not the bottom strand of the ligation products
derived from the first portion, and part of the bottom strand
but not the top strand of the ligation products derived from
the second portion; sequencing at least some of the ampli-
fication products to produce a plurality of top strand reads
and a plurality of bottom strand reads; and counting the
number of STR repeats in a sequence read. A kit for
performing the method is also provided.

16 Claims, 20 Drawing Sheets

Specification includes a Sequence Listing.

